CTCGGTGTCCTCTTGCTGTCCAGCTCTGCAGCCTCCGGCGCGCCCTCCCGCCCACGCCATGGACGCCAAGGTCGTCGCC MetAspAlaLysValValAla

ValleuAlaLeuValLeuAlaAlaLeuCysIleSerAspGlyLysProValSerLeuSerTyrArgCysProCysArgPhe GTGCTGGCCCTGGTGCTGGCGGCGCTCTGCATCAGTGACGGTAAACCAGTCAGCCTGAGCTACCGATGCCGATGCCCTGCCGGTTC

(241)PheGluSerHisIleAlaArgAlaAsnValLysHisLeuLysIleLeuAsnThrProAsnCysAlcLeuGlnIleValAla TTCGAGAGCCACATCGCCAGAGCCAACGTCAAGCATCTGAAAATCCTCAACACTCCAAACTGTGCCCTTCAGATTGTTGCA

ArgleulysAsnAsnAraGlnValCysIleAspProlysLeulysTrpIleGlnGluTyrLeuGluLysAlaLeuAsn : GGCTGAAGAACAACAACAGACAAGTGTGCATTGACCCGAAATTAAAGTGGATCCAAGAGTACCTGGAGAAAGCTTTAAAC

A A GTA A GCA CA A CA GCC CAA A GGA CTTTC CA GTA GA CCC CCGA GGA A GGCT GA CATC CGT GGGA GA TGCA A GGGCA GTGGT

GACACTCC GCCATAGCATATGGTACGATATTGCAGCTTATATTCATCCCTGCCCTCGCCCGGGGTGCACATTGGAGCTTTTATA ACTGGGGTTTTTCTAAGGAATTGTATTACCCTAACCAGTTAGCTTCATCCCCATTCTCCTGATCCTGATCTTCATTTAAA

Fig. 1

(1051) TCCAAACGCATGCTTCATCTGACTTCCGCTTCTCACCTCTGTAGCCTGACGGACCAATGCTGCAATGGAAGGGAGGAGTA C G G T G G C T T T G C A G G G G G C C C A G A A A A C C T T C C A C C A G G A G T C C G A G G A C G C T G C C T G T C C T G C A G G G G G C G C T C C A C A C A T G C C T T G T C C T G A G T C A A C A C A C A G A G G G A G G C T C C T T T A T C C A G T T C A G T G C C A G A GA A T G G A G C C A G A C C T G C G A T A A T G T G A G A A C C T A G A T T T A C C C A C A A A C A C A G A G T T A A T C A T A A T C A T A <u>A A C G G A A G T T T A A A T G G A CTTT G G A CTTT G G T A T T G T C C C T G G T C C T A T T T C A A C A G T G G C T C T A T G G G C T C T G</u> <u>ATCGAATATCAGTGATGAAAATAATAATAATAATAATAATAACGAATAAGCCAGAATCTTGCCATGAAGCCACAGTGGGGA</u> TTCTGGGTTCCAATCAGAAATGGAGACAAGATAAAACTTGCATACÄTTCTTACGATCACAGACGGCCCTGGTGGTTTTTGG TAA CTATTTA CAA GG CA TTTTTTA CA TA TTTTT GT G CA CTTTTTA TG TTT G GA GA GA CAAA TG TTT CA GA TA (1699) TTGTAAAGAAATATATATAAAATGTATTGTAGCTTTCCGGTGTCAGCCACGGTGTGTTTTTCCACTTGGAATGAA GGT CGGGA A GCTT CCTTTA GA A GTGA TCCCTGA A GCTGTGCTCA GA GA CCCTTT CCTA GCC GTT CCTGCTCT CTT GCT GC TA TTT GTA GT CA A TT CA TA TA TTT GA A GT GGA GC CA TA GTAAT GC CA GTA GA TA TCT CTA TGA TCTT GA GC TA CT G G C A A C

Fig. 1 (Continued)

A

B

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CHO cells

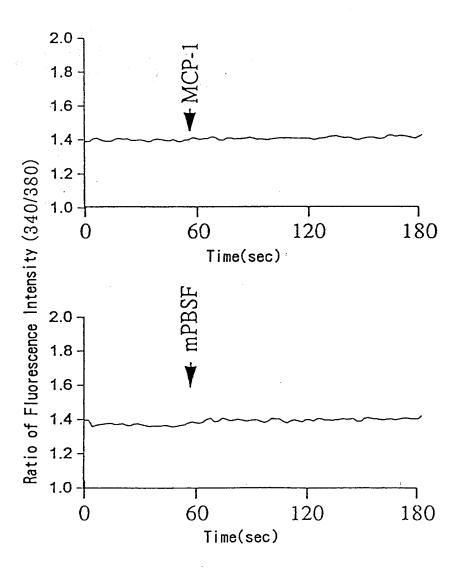


Fig. 3

CHO cells (CC CKR2B+)

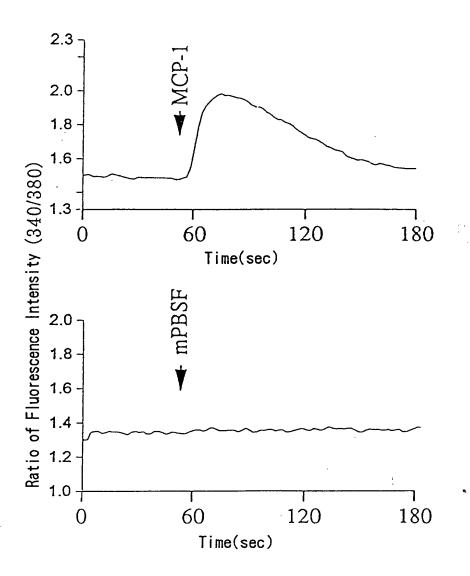


Fig. 4

CHO cells (mPBSF/SDF-1R+)

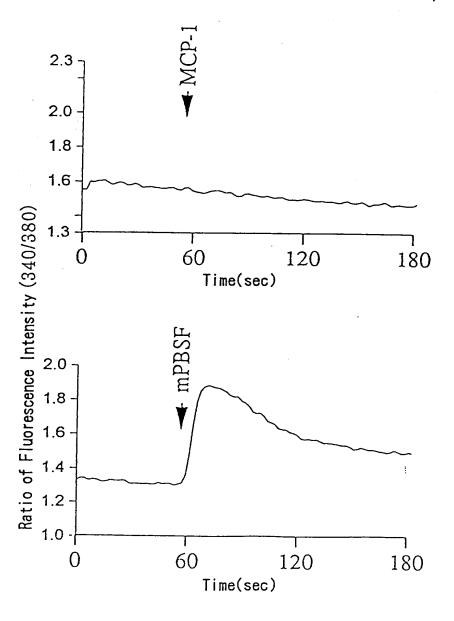


Fig. 5

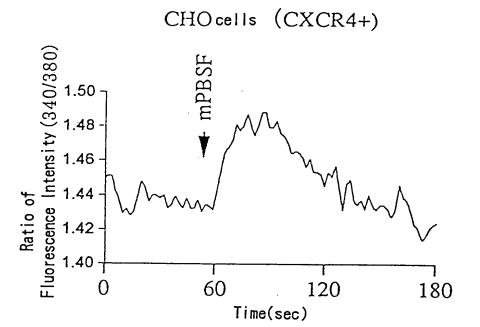


Fig. 6

CHOcells (mPBSF/SDF-1R+)

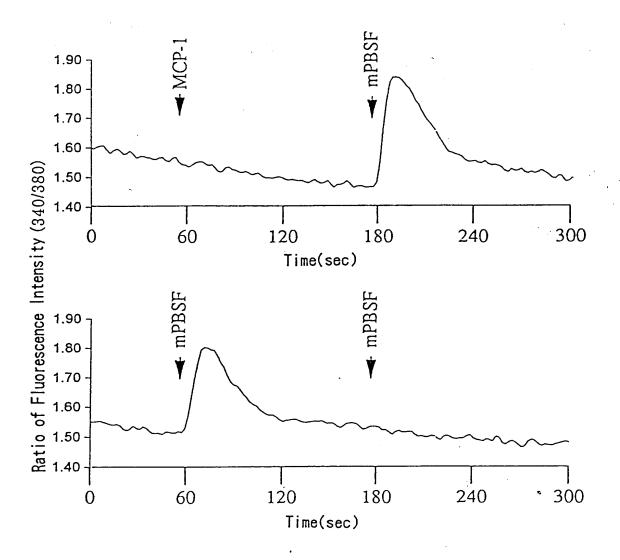
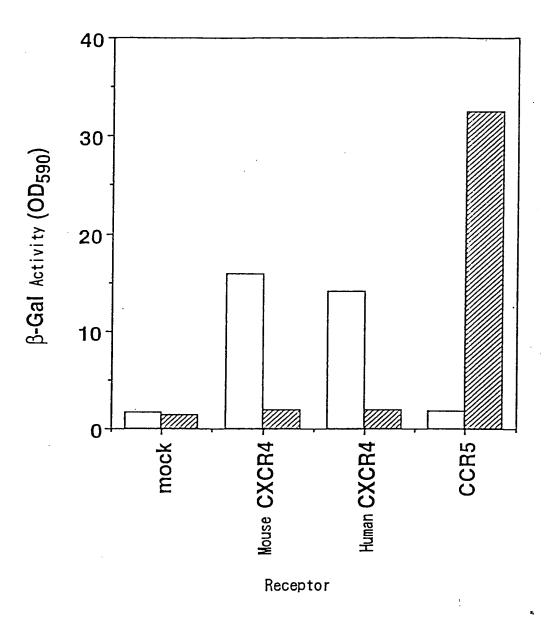


Fig. 7



- ☐ Env (NL432)
 (T-cell-line-tropic strain)
- ☑ Env (SF162) (Macrophage-tropic strain)

Fig. 8

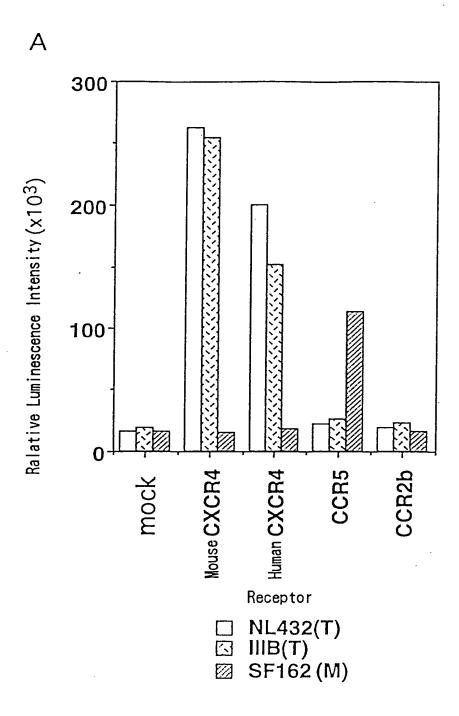


Fig. 9

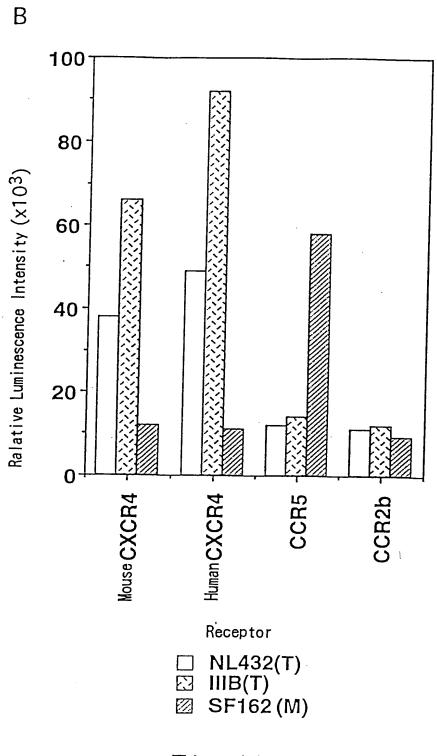
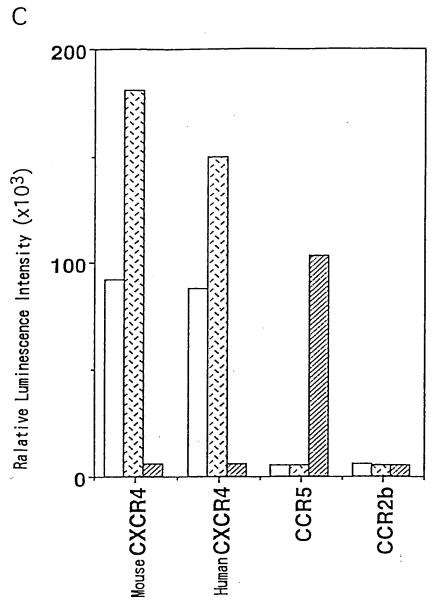


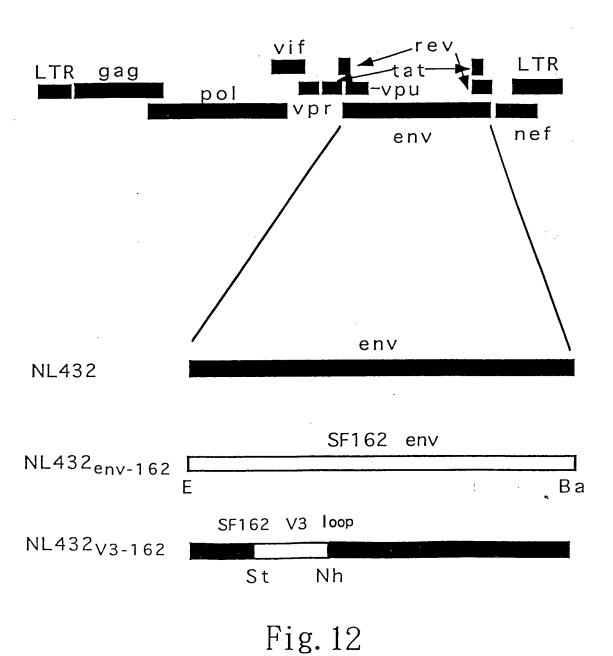
Fig. 10



Receptor

- NL432(T) IIIB(T) SF162 (M)

Fig. 11



1 3 / 1 4

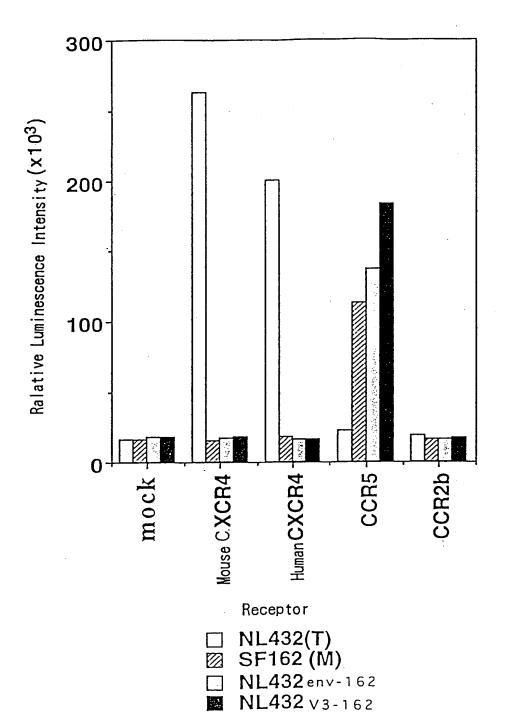


Fig. 13